

Introduction to Botany. Lecture 32

Alexey Shipunov

Minot State University

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Outline

1 Questions and answers

2 Methods of taxonomy

- Expertise
- Cladistics
- Likelihood
- Phenetics

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1 Questions and answers

2 Methods of taxonomy

- Expertise
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- Phenetics

Previous final question: the answer

Is protonema haploid or diploid?

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Is protonema haploid or diploid?

- Haploid

Methods of taxonomy

Expertise

Experts

- Experts produce classifications based of their exclusive knowledge about groups. First taxonomic expert was Carolus Linnaeus (XVIII century).
- Experts use variety of methods, including phenetics, cladistics, general evolutionary approach, their ability to reshape available information and their intuition.
- Their goal is to create the “mind model” of diversity and then convert it to classification.
- In plant taxonomy, Robert Thorne and Armen Takhtajan (deceased in 2009) are most advanced experts

Methods of taxonomy

Cladistics

Steps 1–4

- 1 The goal of analysis is creation of evolutionary history tree (“cladogram”) which become a basis of classification
- 2 We need to start with determining “players”—all subtaxa of bigger group. In our case, it will be three families:

Alphaceae

Betaceae

Gammaceae

- 3 Create descriptions of these three groups:
Alphaceae: Flowers red, petioles short, leaves whole, spines absent
Betaceae: Flowers red, petioles long, leaves whole, spines absent
Gammaceae: Flowers green, petioles short, leaves dissected, spines present
- 4 Separate individual characters (we will need $2N + 1$ characters where N is number of studied taxa):
 - (1) **Flower color**
 - (2) **Petiole size**
 - (3) **Dissection of leaves**
 - (4) **Presence of spines**

Step 5: character coding

- 5 **Polarization of characters:** every characters should have at least two characters states where 0 is a primitive, **plesiomorphic** state, 1 is advanced, **apomorphic** state:
- (1) Flower color green—0; red—1
 - (2) Petiole size small—0; big—1
 - (3) Dissection of leaves absent—0; present—1
 - (4) Absence of spines—0; spines present—1
- 5a These states are usually applied on the base of:
- (a) Historical evidence (e.g., from fossils)
 - (b) Developmental evidence
 - (c) Comparative evidence (from all available taxa)
- 5b If we do not have this information, we need to find **outgroup** which is primitive by definition. In our case, we will employ outgroup:
Omegaceae: Flowers green, petioles short, leaves whole, spines absent.

Step 6: character table

6 Character table

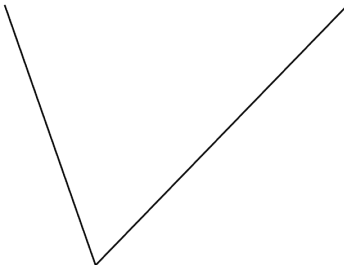
	1	2	3	4
Alphaceae	1	0	0	0
Betaceae	1	1	0	0
Gammaceae	0	0	1	1

[Omegaceae has all zeroes]

Step 7: starting the tree

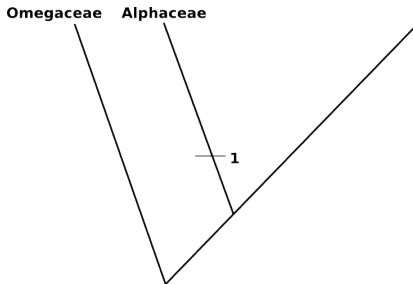
7 Tree is always started from outgroup:

Omegaceae



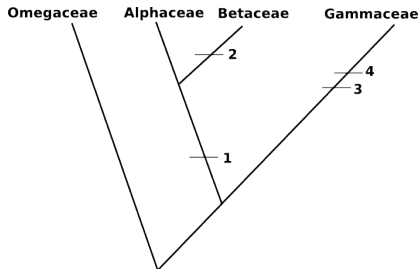
Step 8: first branch

- 8 Then, the most primitive ingroup (Alphaceae) is attached as a first branch:



Step 9: tree is growing

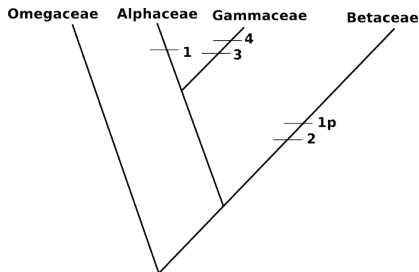
- 9a Then, the more and more advanced taxa are attached. If there is a choice, we can end up with multiple trees. In our case, Betaceae and Gammaceae have equal number of synapomorphies but Betaceae have only one character different from Alphaceae so we attach it there, and finally we attach Gammaceae:



The tree has 4 evolutionary events (length= 4)

Step 10: principle of parsimony

- 9a If we attach taxa in other way (saying, Gammaceae to Alphaceae), the resulted tree will be one step longer:



“p” are parallel characters (homoplasies). There are five events (length= 5).

- 10 We need to choose the shortest, most **parsimonous** tree. Second tree has 5 events, first tree has 4 events. Consequently, we prefer the first tree. Many computer programs produce all possible trees and then choose shortest.

Step 11: resulted classification

- 11 We can now use chosen tree as a source of classification,
e.g.:

Order Alphales

1. Family Alphaceae
2. Family Betaceae

Order Gammales

1. Family Gammaceae

Methods of taxonomy

Likelihood

Likelihood

- Likelihood methods are based on evolutionary models (how characters are evolving, what is a probability of transformation)
- This methods is especially applicable for the analysis of DNA sequences

Methods of taxonomy

Phenetics

Steps 1–6

- 1 The goal of phenetics (or numerical analysis) is creation of dendrogram which become a basis of classification.
Phenetics consider characters as **all equal** and **do not employ any evolutionary assumptions**.
- 2–4 Same as in cladistics: (2) decide which taxa we will need, (3) assess their descriptions, (4) extract characters
- 5 Similar to cladistics, but codes (0 and 1) may be specified arbitrarily, and we do not need outgroup
- 6 Character table is the same

Step 7: matrix of similarity

7 Matrix (or table) of similarity

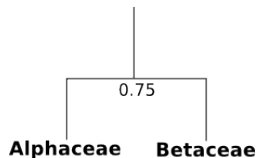
	Alphaceae	Betaceae	Gammaceae
Alphaceae	1		
Betaceae	0.75	1	
Gammaceae	0.25	0	1

Every cell has a value of similarity K :

$$K = \frac{\text{number of matching characters}}{\text{number of all characters}}$$

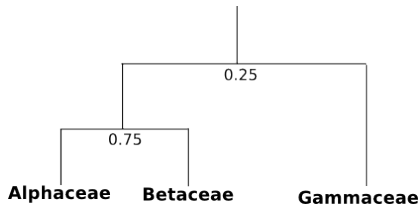
Steps 8: starting a dendrogram

- 8 First, we need to connect the closest taxa, Alphaceae and Betaceae:



Step 9: making a dendrogram

- 9 Then attach other taxa which are closest to to previous group:



Step 10: classification

- 10 Betaceae and Alphaceae are closer, so we can unite them in one order:

Order Alphales

1. Family Alphaceae
2. Family Betaceae

Order Gammales

1. Family Gammaceae

Summary

- Expert methods are based on the creation of mind models of diversity
- Cladistic methods are based on character polarization and parsimony
- Phenetic methods are based on equality of characters and similarity matrix

Final question (3 points)

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Why our cladistic and phenetic classifications are identical?

For Further Reading



Th. L. Rost, M. G. Barbour, C. R. Stocking, T. M. Murphy.
Plant Biology. 2nd edition.
Thomson Brooks/Cole, 2006.
Chapter 18.5.